

CLAIMS

What is claimed is:

1. A method of determining small RNA transcriptional activity comprising:
 - obtaining a small RNA sample;
 - 5 hybridizing the small RNA or nucleic acids derived from the RNA with an oligonucleotide probe array, wherein the oligonucleotide probe array contains at least 10,000 perfect match (PM) probes, each of the perfect match probes targeting a different transcript sequence from a region of a genome; and
 - determining that a genomic sequence is transcribed if the probe against the 10 genomic sequence is hybridized with a target.
2. The method of Claim 1 wherein the region of the genome is at least 20 MB
3. The method of Claim 2 wherein the region of the genome is at least 50 MB.
4. The method of Claim 3 wherein the region of the genome is 25% of the DNA sequences in a chromosome.
- 15 5. The method of Claim 4 wherein the region of the genome is 50% of the DNA sequences in a chromosome.
6. The method of Claim 5 wherein the region of the genome is the DNA from a chromosome.
7. The method of Claim 6 wherein the region of the genome is the DNA 20 sequence from the entire genome.
8. The method of Claim 2 wherein the probes target the transcript sequences from the genome at a resolution of at least 100 bps.

9. The method of Claim 8 wherein the probes target the transcript sequences from the genome at a resolution of at least 30 bps.
10. The method of Claim 9 wherein the probes target the transcript sequences from the genome at a resolution of at least 10 bps.
- 5 11. The method of Claim 10 wherein the probes target the transcript sequences from the genome at the resolution of 1 bp.
12. The method of Claim 2 wherein the small RNA sample is obtained from the nuclei.
- 10 13. The method of Claim 2 wherein the small RNA sample is obtained from the cytoplasm.
14. The method of Claim 13 wherein the oligonucleotide probe array contains at least 100,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.
- 15 15. The method of Claim 14 wherein the oligonucleotide probe array contains at least 500,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.
16. The method of Claim 15 wherein the oligonucleotide probe array contains at least 800,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.
- 20 17. The method of Claim 2 wherein oligonucleotide array further comprises mismatch (MM) probes, wherein each of the mismatch probes is different from a perfect match probe in one base.

18. The method of Claim 17 wherein the mismatch probes is different from the perfect match probe in a middle position.
19. The method of Claim 2 wherein the perfect match probes are targeting transcripts from non-repetitive sequence of the genome.
- 5 20. A method for comparing the small RNA transcriptional activity of two biological samples comprising:
 - obtaining a first small RNA sample;
 - obtaining a second small RNA sample;
 - hybridizing the first and second small RNA samples or nucleic acids derived
- 10 from the first and second small RNA with an oligonucleotide probe array wherein the oligonucleotide probe array contains at least 10,000 perfect match (PM) probes, each of the perfect match probes targeting a different transcript sequence from a region of a genome;
- 15 determining, for each of the first and second sample, that a genomic sequence is transcribed if the probe against the genomic sequence is hybridized with a target; and
- comparing the transcribed sequences between the first and second sample.